

Fig. 1

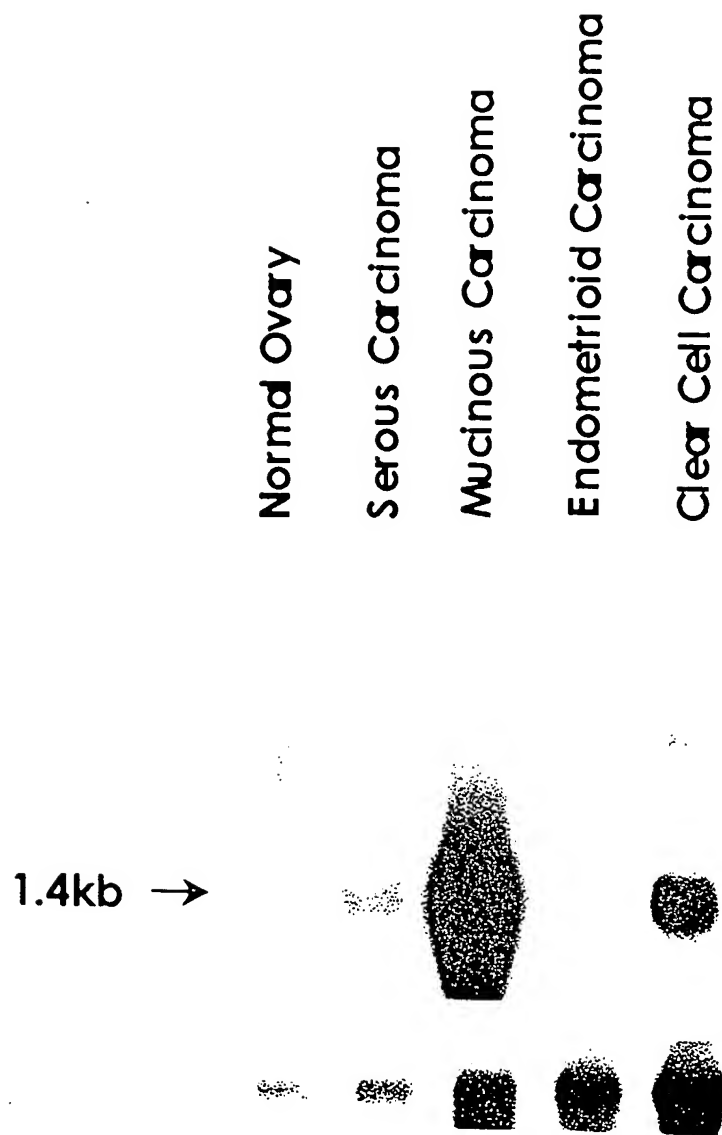


Fig. 2A

FETAL

Brain

Lung

Liver

Kidney



Fig. 2B

ADULT

Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
P.B. Leukocyte *

← TADG14



← β -tubulin

C

* P.B. : Peripheral Blood

Fig. 2C

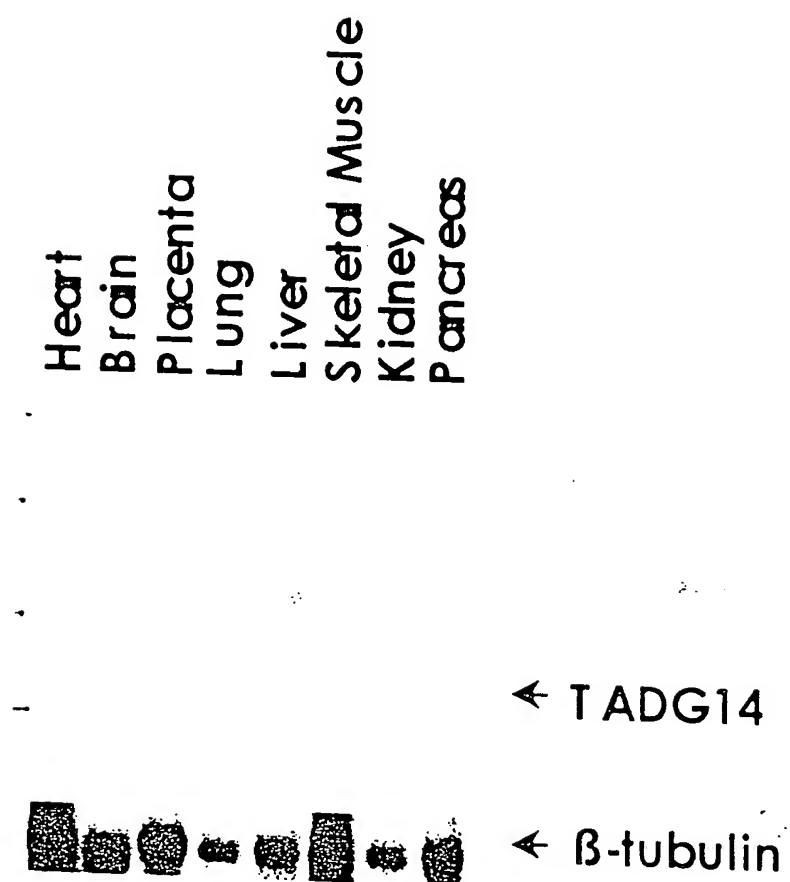


Fig. 2D

1 CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAACCTCAAATGGAAGAAATACCTTATGAATGTAAGAAATGTAGGGGGTCA 80
81 TGGCTTGTAATTTACACAGTGTAAATGAAACCATCCTAGAGGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAG 160
161 CAAGCAAGAAAGGCTCCAGTGTCAAGGTAGTTTCAGCTCTTACAGGATATAAAACAGTCCATACCTTGAGAGAAAAAACTTA 240
241 GATCTGAGTGTAGTGAATGTGAAGCAAATCTTTCAAATCAGTAGACATTTCTTGGACATAAAACACAGATGAGGAAAGGG 320
321 GTTCAAATTAGAAGTTACGTAATACCATCAGAAAGTTTCATGTTGGTAAATTTCTTACTAGAAATGTAGGAAATTCAG 400
401 GTATAGCTTTGAATCCCAATTACACATTTGGTCAAGTGGGAAACTAAGGGCTCCAAACAGGCAAATTCAGGGAGGATAGGT 480
481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTTACCATGGGACGCCCCCGACCTCGTGGCGCAAGACGTGGATGTTCCCTG 560
M G R P R P R A A K T W M F L
561 CTCTTGCTGGGGAGCCTGGCAGGACACTCCAGGGCACAGGAGGACAAGTGTGTTGGGGGTTCATGAGTGCCCAACCCCA 640
L L L G G A W A G H S R A Q E D K V L G G H E C Q P H
641 TTCCGACGCCTTGGCAGGCGGCCTTGTTCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCC 720
S Q P W Q A A L F Q G Q Q L L C G G V L V G G N W V L
721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCTGGGAGACCCACAGCCCTACAGAAATAAAGATGGCCACAG
T A A H C K K P K Y T V R L G D H S L Q N K D G P E
801 CAAGAAATACCTGTGTTCACTCCACACCCCTGTCTACAACAGCAGCGATGTGGAGGACCACCAACCATGATCTGAT 880
Q E I P V Q S I P H P C Y N S S D V E D H N H D L M
881 GCTTGTTCAACTGCGTGACCGATCCCTGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTTGCACCCAGCCTG 960
L L Q L R D Q A S L G S K V K P I S L A D H C T Q P G
961 GCCAGAAGTGCACCGTCTCAGGCTGGGCACTGTCAACAGTCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAA 1040
Q K C T V S G W G T V T S P R E N F P D T L N C A E
1041 GTAAAAATCTTTCCCCAGAGAAGTGTGAGGATGCTTACCCGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAG 1120
V K I F P Q K K C E D A Y P G Q I T D G M V C A G S S
1121 CAAAGGGGCTGACACGTGCGAGGGCGATTCTGGAGGCCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGG 1200
K G A D T C Q G D S G G P L V C D G A L Q G I T S W G
1201 GCTCAGACCCCTGTGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGTACCTGGACTGGATCAAGAAGATC 1280
S D P C G R S D K P G V Y T N I C R Y L D W I K K I
1281 ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACGGAATTC SEQ ID NO. 7
I G S K G * SEQ ID NO. 6

 = Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

 = Poly - adenylation signal

 = Conserved nt of catalytic triad

O = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Fig. 3A

hHk2	~~~~~MW	FLVLCIALSL	GCTGAAPPIQ	SRTVGGWECE	QHSQPWQAAL	42
hPSA	~~~~~MW	VPVFLTLVS	TWIGAAPLIL	SRTVGGWECE	KHSQPWQVLV	42
mNeur	MGRPPCAIQ	PWILTLTFMG	AWAGLTRAQG	SKILEGRECI	PHSQPWQAAL	50
hTADG14	MGRPRPRAAK	TWMFLLELGG	AWAGHSRAQE	DKVLGGHECQ	PHSQPWQAAL	50
hProm	~~~~~MKK	LMVLSLIAA	AWA...EEQ	NKLVHCGPCE	KTSHPYQAAL	39
hHk2	YHFSTFQCGG	ILVHRQWVLT	AAHCISDNMQ	LWLGRHNLFD	DENTAQFVHV	92
hPSA	ASRGRAVECG	VLVHPQWVLT	AAHCIRNKSV	ILLGRHSLFH	PEDTGQVFQV	92
mNeur	FQGERLICCG	VLVGDRWVLT	AAHCKKQKYS	VRLGDHSLQS	RDQPEQEIQV	100
hTADG14	FQGOQLLCCG	VLVGGNWVLT	AAHCKKPKYT	VRLGDHSLQN	KDGPEQEIPIV	100
hProm	YTSCHLLCCG	VLIHPLWVLT	AAHCKKPNLQ	VFLGKHNLERQ	RESSQEQSSV	89
hHk2	SESFPHPGFN	MSLLENHTRQ	ADEDYSHDLM	LLRLTEPADT	ITDAVKVVEL	142
hPSA	SHSFPHPLYD	MSLLKNRFLR	PGDDSSHDEM	LLRLSEPAE.	LTDAVKVMDL	141
mNeur	AQSIQHPCYN	NS.....	NPEDHSHDIM	LLRLQNSAN.	LGDKVKPVQL	141
hTADG14	VQSIQHPCYN	SS.....	DVEDHSHDEM	LLRLQRDQAS.	LGSKVKPISL	141
hProm	VRAVIHBDY.	DAASHDQDIM	LLRLARPAK.	LSELIQPLPL	127
hHk2	PTQEREVCST	CLASGWCISIE	PENFSEPDLL	QGVDLKILPN	DECEKAHVQK	192
hPSA	PTQEPALCIT	CYASGWCISIE	PEEFLTPKKL	QGVDLHVISN	DVCAQVHPQK	191
mNeur	ANLCPKVQOK	CIISGNGTIVT	SPQENFPNTL	NCAEVKITYSQ	NKGERAYPGK	191
hTADG14	ADHCCTQPGOK	CTVSGWGTIVT	SPRENFPDTE	NCAEVKIFPQ	KKCEDAYPGQ	191
hProm	ERDCSANTTS	CHILGWGKTA	D..GDFPDIT	QCAIYIHLVSR	EECEHAYPGQ	175
hHk2	VTDFMLCVGH	LEGKDTCTVG	DSGGPLMCDG	VLOGVTWVG	VPCGTPNKPS	242
hPSA	VTKFMLCAGR	WTGKSTCTSG	DSGGPLVONG	VLOGITWVG	EPCALPERPS	241
mNeur	ITEGMVCAGS	SN.GADTCOG	DSGGPLVCDG	MLOGITWVG	DPCGKPEKPG	240
hTADG14	ITDGMVCAGS	SK.GADTCOG	DSGGPLVCDG	ALOGITWVG	DPCGRSDKPG	240
hProm	ITQNMLCAGD	EKYGKDSCTCG	DSGGPLVCGD	HLRGLVSWGN	IPCGSKEKPG	225
hHk2	VAVRVLSYVK	WIETIAENS	SEQ ID NO: 9			262
hPSA	LYTKVAVHVRK	WIKDTIVANP	SEQ ID NO: 10			261
mNeur	VYTKICRYTT	WIKKTMNDRD	SEQ ID NO: 8			260
hTADG14	VYTNICRYLD	WIKKIIGSKG	SEQ ID NO: 7			260
hProm	VYTNVCRYTN	WIKKTIQAK-	SEQ ID NO: 11			244

Fig. 3B

201 Prom WVLTA AHC KK PNLQV...F LGKHNLRQRE SSQEQSSVVR AVIHPDY... 250
 Tag14 WVVTAAHC KK PKYTV...R LGDHSLQNKD GPEQEIPVVQ SIPHPCY...
 Try1 WVVSAGHC YK SRIQV...R LGEHNIEVLE GNEQFINAAK IIRHPQY...
 Scce WVLTA AHC KM NEYTV...H LGSDTLGDRR A..ORIKASK SFRHPGY...
 Heps WVLTA AHC FP ERNRVLSRWR VFAGAVAQAS PHGLGLGVQA VVYHGGYLF 250

251 Prom ... DAASHDQ DIMLL RLARP AKLSELIQPL PLERDCSA.. NTTSCHILGW 300
 Tag14 NSSDVEDHNH DLMLL QLRDQ ASLGSVKVPI SLADHCTQ.. PGQNCVTSWG
 Try1 ... DRKTLNN DIMLI KLSSR AVINARVSTI SLPTAPPA.. TGTKCLISGW
 Scce ST...QTHVN DLMLV KLNSQ ARLSSMVKKV RLP SRCEP.. PGTTCTVSGW
 Heps RDPNSEENSN DIALV HLSSP LPLTEYIQPV CLPAAGQALV DGKICTVTGW 300

301 Prom GKTAD..GDF PDTIQCAYIH LVSREECEHA ..TPGQITQN MLCAGDEKYG 350
 Tag14 GTVTSPRENF PDTLNCAEVK IFPQKKCEDA ..YPGQITDG MVCAGSSK.G
 Try1 GNTASSGADY PDELQCLDAP VLSQAKCEAS ..YPGKITSN MFCVGFLEGG
 Scce GTTTSPPDTF PSDLMCVDVK LISPQDCTKV ..YKDLLENS MLCAGIPDSK
 Heps GNTQYYGQQ. AGVLQEARVP IISNDVCNGA DFYGNQIKPK MFCAGYPEGG 350

351 Prom KDSCQ GDSCG SEQ ID No. 1
 Tag14 ADTCQ GDSCG SEQ ID No. 2
 Try1 KDSCQ GDSCG SEQ ID No. 3
 Scce KNACN GDSCG SEQ ID No. 4
 Heps IDACQ GDSCG SEQ ID No. 5
 PRIMER

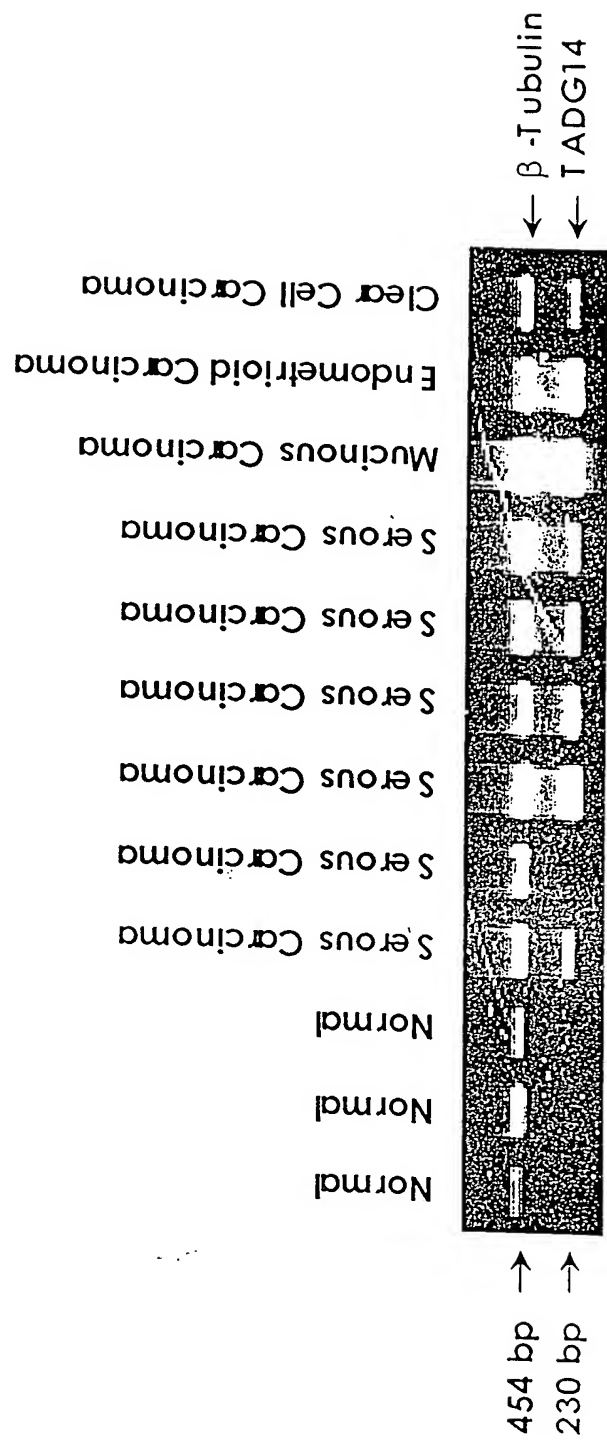


Fig. 5A

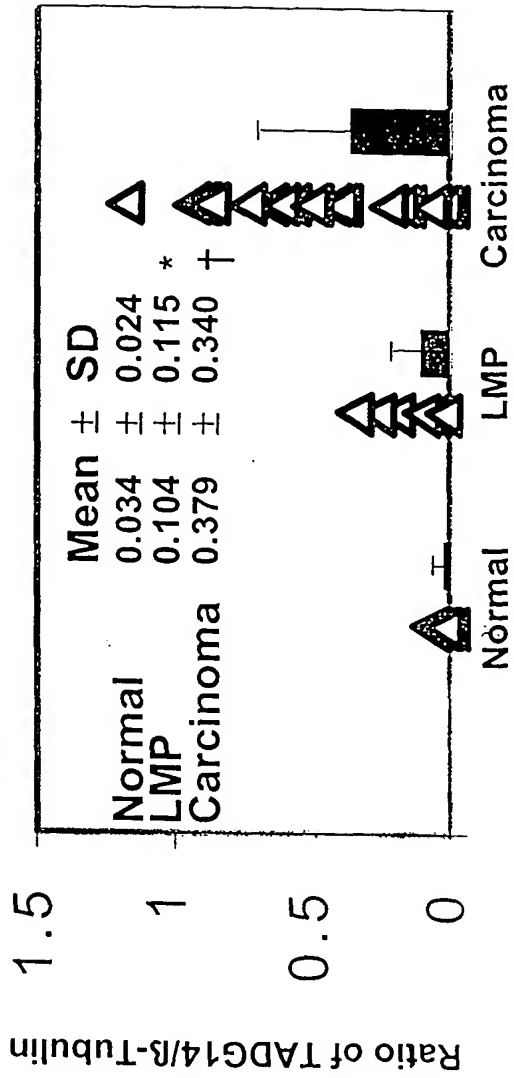


Fig. 5B

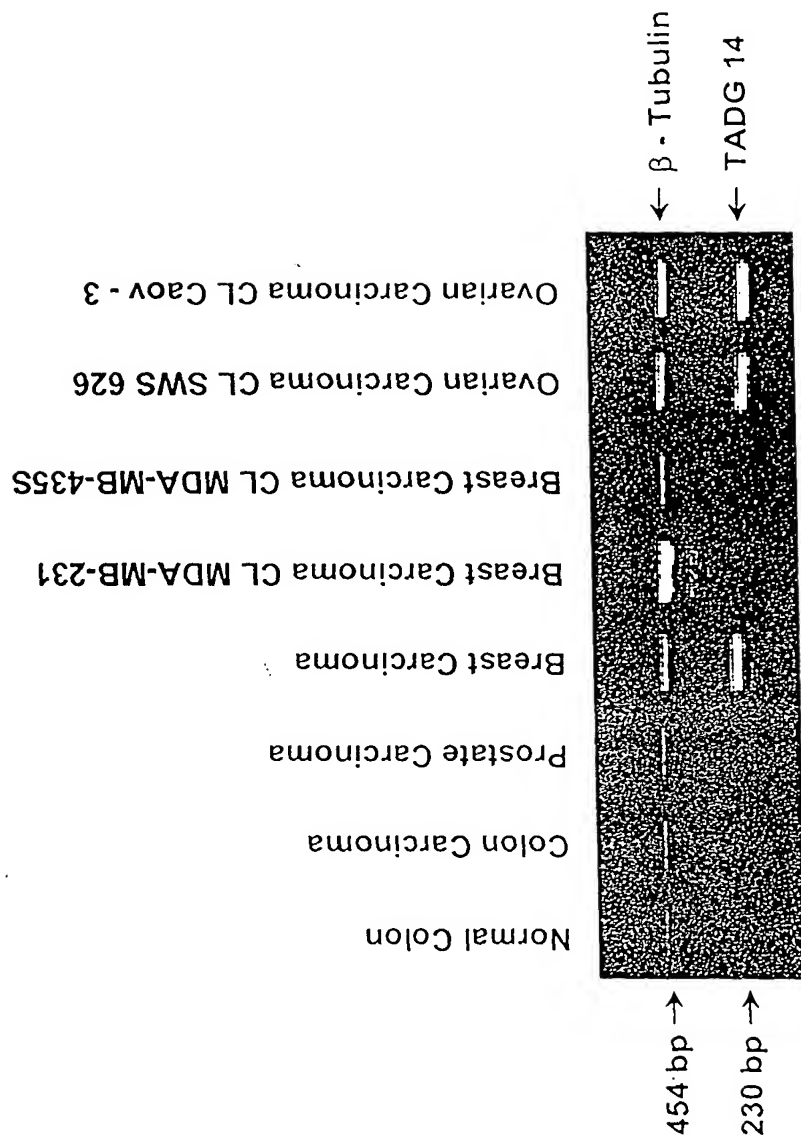


Fig. 6

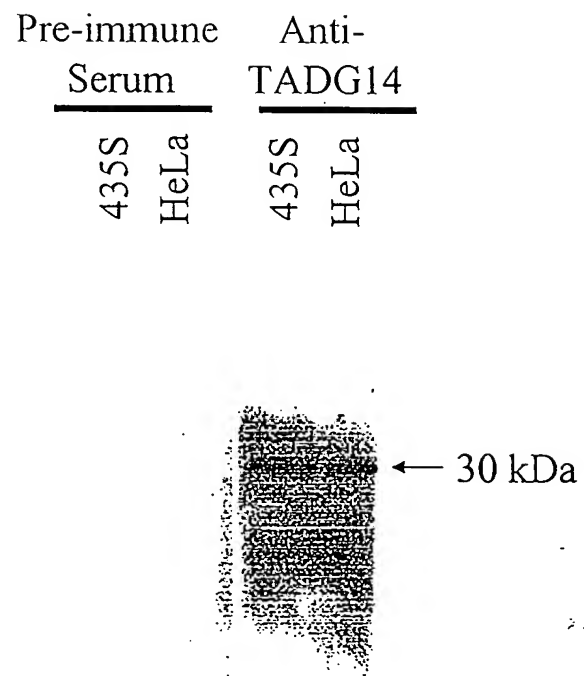
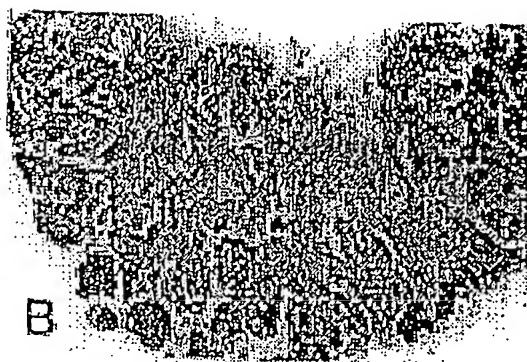


Fig. 7



A

Fig. 8A



B

Fig. 8B



C

Fig. 8C

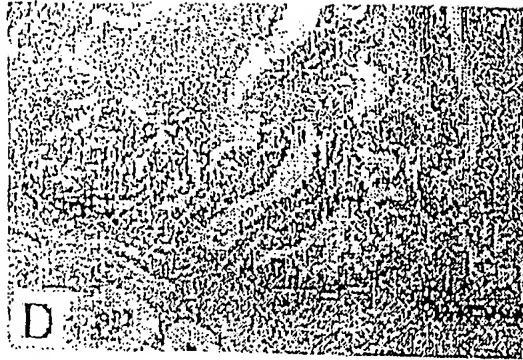


Fig. 8D



Fig. 8E

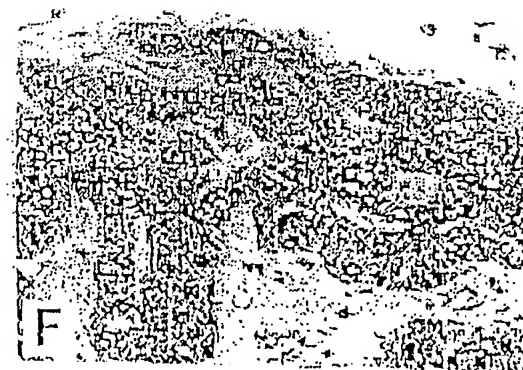


Fig. 8F

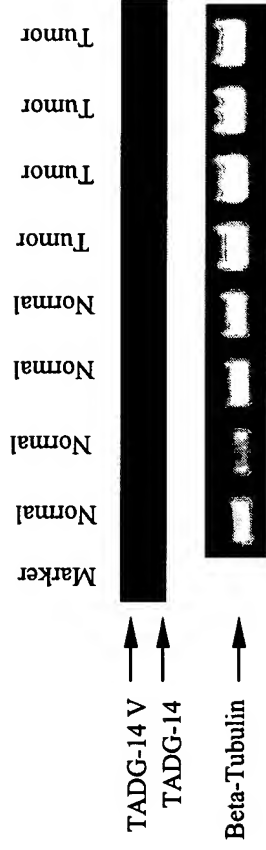


Fig. 9

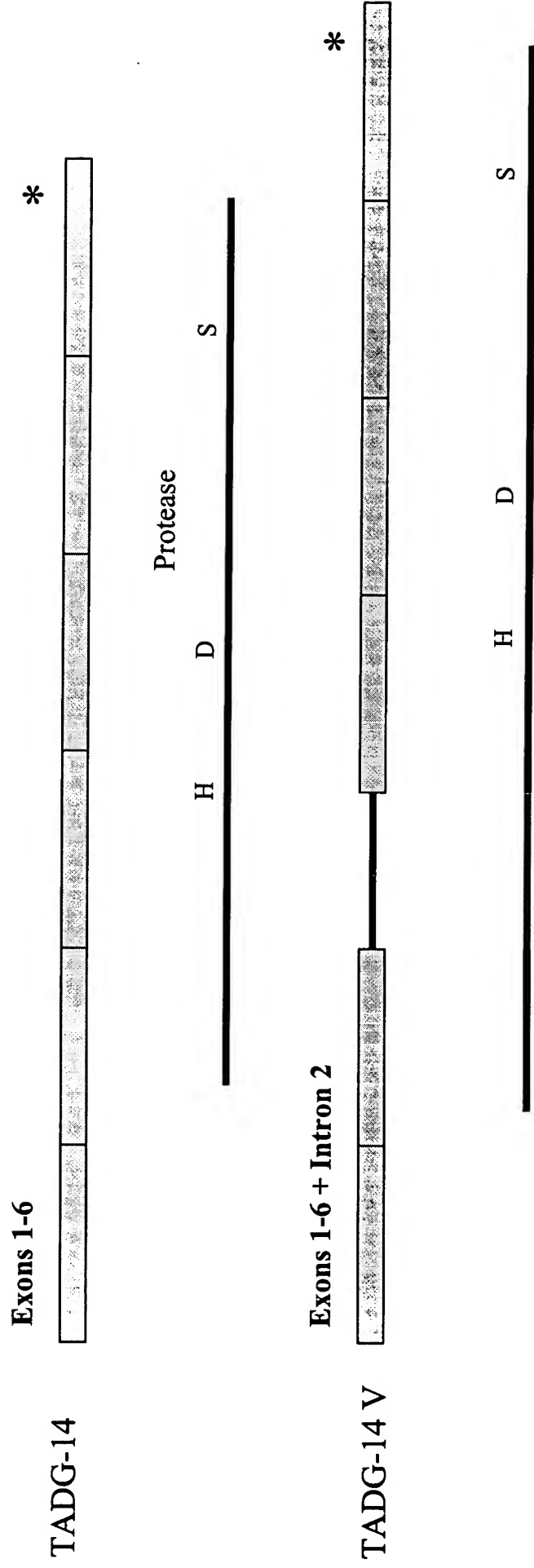


Fig. 10

Tadg 14	MGRPRPRAAK	TWMFLLLLLG	AWA.....
Tadg 14 V	MGRPRPRAAK	TWMFLLLLLG	AWAACGSLDL	LTKLYAENLP CVHLNPQWPS
Tadg 14GH	SRAQEDKVLG	GHECQPHSQP WQAALFQGQQ
Tadg 14 V	QPSHCPRGWR	SNPLPPAAGH	SRAQEDKVLG	GHECQPHSQP WQAALFQGQQ
Tadg 14	LLCGGVLVGG	NWVLTAAHCK	KPKYTVRLGD	HSLQNKDGPE QEIPVVQSIP
Tadg 14 V	LLCGGVLVGG	NWVLTAAHCK	KPKYTVRLGD	HSLQNKDGPE QEIPVVQSIP
Tadg 14	HPCYNSSDVE	DHNHDLMLLQ	LRDQASLGSK	VKPISLADHC TQPGQKCTVS
Tadg 14 V	HPCYNSSDVE	DHNHDLMLLQ	LRDQASLGSK	VKPISLADHC TQPGQKCTVS
Tadg 14	GWGTVTSPRE	NFPDTLNCAE	VKIFPQKKCE	DAYPGQITDG MVCAGSSKGA
Tadg 14 V	GWGTVTSPRE	NFPDTLNCAE	VKIFPQKKCE	DAYPGQITDG MVCAGSSKGA
Tadg 14	DTCQGDSSGP	LVCDGALQGI	TSWGSDPCGR	SDKPGVYTNI CRYLDWIKKI
Tadg 14 V	DTCQGDSSGP	LVCDGALQGI	TSWGSDPCGR	SDKPGVYTNI CRYLDWIKKI
Tadg 14	IGSKG (SEQ ID NO. 7)			
Tadg 14 V	IGSKG (SEQ ID NO. 75)			

Fig. 11